

## AMENDMENTS TO THE CLAIMS:

Claims 1-40, 42 and 50 are canceled without prejudice or disclaimer. Claims 41, 44 and 45 are amended. Claims 51-57 are added. The following is the status of the claims of the above-captioned application, as amended.

### Claims 1-40 (Canceled)

Claim 41 (Currently amended.) A variant of an alpha-amylase, said variant comprising an amino acid sequence having at least 90% homology to SEQ ID NO:8, comprising an alteration at a position corresponding to position 170 in SEQ ID NO:8, and comprising an alteration at one or more positions selected from the group of 49, 60, 104, 132, 161, 176, 179, 180, 181, 183, 200, 203, 204, 207, 212, 237, 239, 250, 280, 298, 318, 374, 385, 393, 402, 406, 427, 430, 440, 444, 447, and 482 (using SEQ ID NO:8 for numbering), and wherein the variant has alpha-amylase activity.

### Claim 42 (Cancelled)

Claim 43 (Previously presented) The variant of claim 41, which variant comprises an alteration of K170Q.

Claim 44. (Currently amended) The variant of claim 41, which variant comprises an alteration of one or more of the following mutations: T49I; D60N; N104D; E132A,V,P; D161N; ~~K170Q;~~ K176R; G179N; K180T; A181N; D183N; D200N; X203Y; D204S; D207V,E,L,G; X212I; K237P; S239W; E250G,F; N280S; X298Q; L318M; Q374R; E385V; Q393R; Y402F; H406L,W; L427I D430N; V440A; N444R,K; E447Q,K; Q482K using SEQ ID NO: 8 for the numbering.

Claim 45 (Currently amended) The variant of claim 41, wherein the variant has one of the following mutations:

K170Q+D207V+N280S;

~~E132A+D207V;~~

~~D207E+E250G+H406L+L427I;~~

~~D207V+L318M;~~

~~D60N+D207V+L318M;-~~  
~~T49I+E132V+V440A;-~~  
~~T49I+K176R+D207V+Y402F;-~~  
~~Q374R+E385V+Q393R;-~~  
~~N190F+A209V+Q264S;-~~  
~~G48A+T49I+G107A+I201F;-~~  
~~T49I+G107A+I201F;-~~  
~~G48A+T49I+I201F;-~~  
~~G48A+T49I+G107A;-~~  
~~T49I+I201F; T49I+G107A; G48A+T49I;~~  
~~N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444K+E447Q+Q482K;-~~  
~~D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444K+E447Q+Q482K;-~~  
~~D161N+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444K+E447Q+Q482K;-~~  
~~D161N+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+E447Q+Q482K;-~~  
~~N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+E447Q+Q482K;-~~  
~~D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+E447Q+Q482K;-~~  
~~N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N;-~~  
~~D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N;-~~  
~~H406W+D430N; N444K+E447Q+Q482K; E447Q+Q482K;-~~  
~~N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444R+N444K+E447K+Q482K;-~~  
~~D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444R+N444K+E447K+Q482K;-~~  
~~N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W;-~~  
~~D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W;-~~

~~H406W+D430N; N444K+E447K+Q482K; E447K+Q482K;~~  
~~N104D+D161N+A181N+D183N+D200N+D204S+K237P+S239W;~~  
~~N104D+D161N+A181N+D183N+D200N+D204S+K237P;~~  
~~N104D+D161N+A181N+D183N+D200N+D204S;~~  
~~D161N+A181N+D183N+D200N+D204S+K237P+S239W;~~  
~~D161N+A181N+D183N+D200N+D204S+K237P;~~  
D161N+A181N+D183N+D200N+D204S; K237P+S239W; T49I+D60N+E132V+K170Q;  
T49I+D60N+E132A+K170Q; T49I+D60N+E132V+K170Q+K176R;  
T49I+D60N+E132A+K170Q+K176R;  
T49I+D60N+E132V+K170Q+K176R+D207V;  
T49I+D60N+E132A+K170Q+K176R+D207V;  
T49I+D60N+E132V+K170Q+K176R+D207E;  
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E385V+Q393R;

T49I+D60N+E132A+K170Q+K176R+D207V+E250G+N280S+L318M+Q374R+  
E385V+Q393R;  
T49I+D60N+E132V+K170Q+K176R+D207E+E250G+N280S+L318M+Q374R+  
E385V+Q393R;  
T49I+D60N+E132A+K170Q+K176R+D207E+E250G+N280S+L318M+Q374R+E385V+  
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E385V+Q393R+Y402F;  
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T49I+D60N+E132A+K170Q+K176R+D207E+E250G+N280S+L318M+Q374R+E385V+  
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D60N+E132A+K170Q+K176R+D207E+E250G+N280S+L318M+Q374R+E385V+  
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E132A+K170Q+K176R+D207E+E250G;  
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E132V+K170Q+K176R+D207V+E250G+N280S+L318M;  
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E385V+Q393R+Y402F+H406L+L427I+V440A;  
E132A+K170Q+K176R+D207E+E250G+N280S+L318M+Q374R+E385V+  
Q393R+Y402F+H406L+L427I+V440A;  
K170Q+K176R;  
K170Q+K176R+D207V;  
K170Q+K176R+D207E;  
K170Q+K176R+D207V+E250G;  
K170Q+K176R+D207E+E250G;  
K170Q+K176R+D207V+E250G+N280S;  
K170Q+K176R+D207E+E250G+N280S;  
K170Q+K176R+D207E+E250G+N280S+L318M;  
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K170Q+K176R+D207E+E250G+N280S+L318M+Q374R+  
E385V+Q393R+Y402F+H406L;  
K170Q+K176R+D207V+E250G+N280S+L318M+Q373R+  
E385V+Q393R+Y402F+H406L+L427I;  
K170Q+K176R+D207E+E250G+N280S+L318M+Q374R+  
E385V+Q393R+Y402F+H406L+L427I;  
K170Q+K176R+D207V+E250G+N280S+L318M+Q373R+  
E385V+Q393R+Y402F+H406L+L427I+V440A; or  
K170Q+K176R+D207E+E250G+N280S+L318M+Q374R+  
E385V+Q393R+Y402F+H406L+L427I+V440A (using SEQ ID NO: 8 for the numbering).

Claim 46 (Previously presented) The variant of claim 41, wherein the variant is derived from a strain of *B. licheniformis*.

Claim 47 (Previously presented) The variant of claim 41, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 95%.

Claim 48 (Previously presented) The variant of claim 41, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 97%.

Claim 49 (Previously presented) The variant of claim 41, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 99%.

Claim 50 (Canceled)

Claim 51 (New.) A variant of an alpha-amylase, wherein the variant comprises an amino acid sequence having at least 90% homology to SEQ ID NO:8 and a substitution of a Q at a position corresponding to position 170 in SEQ ID NO:8, and wherein the variant has alpha-amylase activity.

Claim 52 (New) The variant of claim 51, wherein the variant has an amino acid sequence which

has a degree of homology to SEQ ID NO: 8 of at least 95%.

Claim 53 (New) The variant of claim 51, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 97%.

Claim 54 (New) The variant of claim 51, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 99%.

Claim 55 (New.) The variant of claim 51, wherein the variant is derived from a *Bacillus licheniformis* alpha-amylase.

Claim 56. (New.) A variant *Bacillus licheniformis* alpha-amylase, wherein the variant comprises an amino acid sequence having at least 90% homology to SEQ ID NO:8 and an alteration of a Q at a position corresponding to position 170 in SEQ ID NO:8, and wherein the variant has alpha-amylase activity.

Claim 57. (New.) A variant *Bacillus licheniformis* alpha-amylase, wherein the variant consists of an alteration of a Q at a position corresponding to position 170 in SEQ ID NO:8, and wherein the variant has alpha-amylase activity.